AMENDMENTS TO THE CLAIMS

Please amend claims 23-25, 28-30 and 58 as shown in the following list of claims.

1.-22. (Canceled).

23. (Currently amended) A method for identifying at least one endogenous molecule that differs in abundance between a first cell population and a second cell population, comprising:

(a) comparing a first Fourier Transform Mass Spectrometry (FTMS) peak profile obtained from the first cell population with a second FTMS peak profile obtained from the second cell population, wherein the first peak profile and the second peak profile are obtained independently;

(b) identifying at least one peak that differs in intensity in the first FTMS peak profile relative to the second FTMS peak profile, which said at least one peak corresponds to at least one molecule that differs in abundance between a first cell population and a second cell population; and

(c) identifying said at least one molecule that differs in abundance between the first cell population and the second cell population either directly from mass-to-charge (m/z) ratio of said at least one peak or through additional fragmentation of said at least one molecule;

thereby ~~identifying~~ at least one molecule**[[s]]** that differs in abundance between a first cell population and a second cell population is identified.

24. (Currently amended) A method for identifying at least one endogenous molecule that differs in abundance between a first cell population and a second cell population, comprising:

(a) comparing a first FTMS peak profile obtained from the first cell population with a second FTMS peak profile obtained from the second cell population, wherein the first peak profile and the second peak profile are not obtained concurrently and wherein the first and second cell populations do not contain a label;

(b) identifying at least one peak that differs in intensity in the first FTMS peak profile relative to the second FTMS peak profile, which said at least one peak corresponds to at least one molecule that differs in abundance between a first cell population and a second cell population; and

(c) identifying said at least one molecule that differs in abundance between the first cell population and the second cell population either directly from mass-to-charge (m/z) ratio of said at least one peak or through additional fragmentation of said at least one molecule;

thereby ~~identifying~~ at least one molecule[[s]] that differs in abundance between a first cell population and a second cell population is identified.

25. (Currently amended) A method for identifying at least one endogenous molecule that differs in abundance between a first cell population and a second cell population, comprising:

(a) comparing a first FTMS peak profile obtained from the first cell population with a second FTMS peak profile obtained from the second cell population, wherein the first peak profile and the second peak profile are obtained from whole cell extracts;

(b) identifying at least one peak that differs in intensity in the first FTMS peak profile relative to the second FTMS peak profile, which said at least one peak corresponds to at least one molecule that differs in abundance between a first cell population and a second cell population; and

(c) identifying said at least one molecule that differs in abundance between the first cell population and the second cell population either directly from mass-to-charge (m/z) ratio of said at least one peak or through additional fragmentation of said at least one molecule;

thereby ~~identifying~~ at least one molecule[[s]] that differs in abundance between a first cell population and a second cell population is identified.

26. (Previously presented) The method of claim 25, wherein the whole cell extract is a solvent-extracted cell extract.

27. (Previously presented) The method of claim 25, wherein the whole cell extract is desalted.

28. (Currently amended) The method of any one of claims 23 to27, further comprising:

~~(c)~~ (d) prior to step (a), obtaining the first FTMS peak profile from the first cell population by subjecting said first cell population to FTMS.

29. (Currently amended) The method of any one of claims 23 to27, further comprising:

~~(c)~~ (d) prior to step (a), obtaining the second FTMS peak profile from the second cell population by subjecting said second cell population to FTMS.

30. (Currently amended) The method of claim 28, further comprising:

~~(d)~~ (e) prior to step (a), obtaining the second FTMS peak profile from the second cell population by subjecting said second cell population to FTMS.

31. (Previously presented) The method of any one of claims 23 to 27, wherein the first cell population is a reference cell population and the second cell population is a test cell population.

32. (Previously presented) The method of claim 31, wherein the first and second cell population are of different cell types.

33. (Previously presented) The method of claim 32, wherein the first and second cell populations are of different tissue types from the same organism.

34. (Previously presented) The method of claim 32, wherein the first and second cell populations are of the same tissue type from different organisms.

35. (Previously presented) The method of any one of claims 23 to 27, wherein the first and second cell populations are of the same cell type.

36. (Previously presented) The method of claim 35, wherein the first cell population is a normal cell population and the second cell population is a diseased cell population and wherein the at least one molecule is a marker of the disease.

37. (Previously presented) The method of claim 36, wherein the diseased cell population is a cancerous cell population and wherein the marker is a marker for cancer.

38. (Previously presented) The method of claim 37, wherein the cancerous cell population is a population of melanoma, myeloid leukemia, or carcinoma cells.

39. (Previously presented) The method of claim 38, wherein the carcinoma is lung, breast, ovarian, colon, kidney, prostate, pancreatic, stomach, brain, lymphatic system, thymic, thyroid, adrenal or testicular carcinoma.

40. (Previously presented) The method of claim 36, wherein the diseased cell population is from an individual with cardiovascular disease and wherein the marker is a marker for cardiovascular disease.

41. (Previously presented) The method of claim 40, wherein the diseased cell population is a population of cardiomyocytes, endothelial cells, macrophages, hepatocytes, adipocytes, smooth muscle cells or intestinal cells.

42. (Previously presented) The method of claim 36, wherein the diseased cell population is from an individual with diabetes.

43. (Previously presented) The method of claim 42, wherein the diseased cell population is a population of cardiomyocytes, endothelial cells, macrophages, pancreatic cells, hepatocytes, adipocytes, smooth muscle cells or intestinal cells.

44. (Previously presented) The method of claim 36, wherein the diseased cell population is from an obese individual.

45. (Previously presented) The method of claim 44, wherein the diseased cell population is a population of cardiomyocytes, endothelial cells, macrophages, hepatocytes, adipocytes, smooth muscle cells or intestinal cells.

46. (Previously presented) The method of claim 35, wherein the first cell population has not been subjected to a test agent and the second cell population has been subjected to the test agent.

47. (Previously presented) The method of claim 46, wherein the test agent is a known drug.

48. (Previously presented) The method of claim 46, wherein the test agent is a drug candidate.

49. (Previously presented) The method of claim 46, wherein the test agent is a small molecule.

50. (Previously presented) The method of claim 46, wherein the test agent is a protein.

51. (Previously presented) The method of claim 50, wherein the protein is a hormone, a growth factor, a cytokine, a ligand, or an antibody.

52. (Previously presented) The method of claim 46, wherein the test agent is a nucleic acid.

53. (Previously presented) The method of claim 52, wherein the nucleic acid is an antisense nucleic acid, a triple helix nucleic acid, or a ribozyme.

54. (Previously presented) The method of claim 46, wherein the nucleic acid is a DNA, an RNA, or a DNA-RNA hybrid.

55. (Previously presented) The method of claim 31, wherein the first FTMS peak profile is a historical control.

56. (Previously presented) The method of claim 31, wherein the first FTMS peak profile is a concurrent control.

57. (Previously presented) The method of any one of claims 23 to 27, wherein the first and second cell populations are populations of primary cells from a tissue or organ.

58. (Currently amended) The method of claim ~~5747~~ 57, wherein in the primary cells are primary brain, skin, lung, endothelial, epithelial, adipose, muscle, bone, stomach, colon, spleen, pancreas, kidney, bladder, heart, lymphatic system, blood, or liver cells.